

SEQUENCE LISTING



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<110> Cashman, John R.
Lomri, Nouredine

<120> DNA SEQUENCE ENCODING FLAVIN-CONTAINING MONOOXYGENASE

<130> 16663-1-2

<140> 09/583,310

<141> 2000-05-30

<150> 08/617,671

<151> 1996-03-27

<150> 08/023,843

<151> 1993-02-26

<160> 18

<170> PatentIn Ver. 2.1

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: cDNA probe
complementary to pig liver FMO

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<210> 2

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<213> Artificial Sequence

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complementary to pig liver FMO

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<210> 3
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 <212> DNA
 <213> Artificial Sequence

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 <223> Description of Artificial Sequence: AflIII site of
 5' HLFMO-3 cDNA

<400> 3
 ggtaccacat gtccatgggg aagaaag 27

<210> 4
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Sal I site &
 13 NT seq complementary to 3' end HLFMO-3 cDNA

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<210> 5
 <211> 1599
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 <213> Homo sapiens

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 Ser Ile Arg Ser Cys Leu Glu Glu Gly Leu Glu Pro Thr Cys Phe Glu
 20 25 30
 aag agc aat gac att ggg ggc ctg tgg aaa ttt tca gac cat gca gag 144
 Lys Ser Asn Asp Ile Gly Gly Leu Trp Lys Phe Ser Asp His Ala Glu
 35 40 45

gag ggc agg gct agc att tac aaa tca gtc ttt tcc aac tct tcc aaa	192
Glu Gly Arg Ala Ser Ile Tyr Lys Ser Val Phe Ser Asn Ser Ser Lys	
50 55 60	
gag atg atg tgt ttc cca gac ttc cca ttt ccc gat gac ttc ccc aac	240
Glu Met Met Cys Phe Pro Asp Phe Pro Phe Pro Asp Asp Phe Pro Asn	
65 70 75 80	
ttt atg cac aac agc aag atc cag gaa tat atc att gca ttt gcc aaa	288
Phe Met His Asn Ser Lys Ile Gln Glu Tyr Ile Ile Ala Phe Ala Lys	
85 90 95	
gaa aag aac ctc ctg aag tac ata caa ttt aag aca ttt gta tcc agt	336
Glu Lys Asn Leu Leu Lys Tyr Ile Gln Phe Lys Thr Phe Val Ser Ser	
100 105 110	
gta aat aaa cat cct gat ttt gca act act ggc cag tgg gat gtt acc	384
Val Asn Lys His Pro Asp Phe Ala Thr Thr Gly Gln Trp Asp Val Thr	
115 120 125	
act gaa agg gat ggt aaa aaa gaa tcg gct gtc ttt gat gct gta atg	432
Thr Glu Arg Asp Gly Lys Lys Glu Ser Ala Val Phe Asp Ala Val Met	
130 135 140	
gtt tgt tcc gga cat cat gtg tat ccc aac cta cca aaa aag tcc ttt	480
Val Cys Ser Gly His His Val Tyr Pro Asn Leu Pro Lys Lys Ser Phe	
145 150 155 160	
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Pro Gly Leu Asn His Phe Lys Gly Lys Cys Phe His Ser Arg Asp Tyr	
165 170 175	
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Lys Glu Pro Gly Val Phe Asn Gly Lys Arg Val Leu Val Val Gly Leu	
180 185 190	
ggg aat tcg ggc tgt gat att gcc aca gaa ctc agc cgc aca gca gaa	624
Gly Asn Ser Gly Cys Asp Ile Ala Thr Glu Leu Ser Arg Thr Ala Glu	
195 200 205	
cag gtc atg atc agt tcc aga agt ggc tcc tgg gtg atg agc cgg gtc	672
Gln Val Met Ile Ser Ser Arg Ser Gly Ser Trp Val Met Ser Arg Val	
210 215 220	
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Trp Asp Asn Gly Tyr Trp Trp Asp Met Leu Leu Val Thr Arg Phe Gly	
225 230 235 240	

acc ttc ctc aag aac aat tta ccg aca gcc atc tct gac tgg ttg tac	768
Thr Phe Leu Lys Asn Asn Leu Pro Thr Ala Ile Ser Asp Trp Leu Tyr	
245 250 255	
gtg aag cag atg aat gca aga ttc aag cat gaa aac tat ggc ttg atg	816
Val Lys Gln Met Asn Ala Arg Phe Lys His Glu Asn Tyr Gly Leu Met	
260 265 270	
cct tta aat gga gtc ctg agg aaa gag cct gta ttt aac gat gag ctc	864
Pro Leu Asn Gly Val Leu Arg Lys Glu Pro Val Phe Asn Asp Glu Leu	
275 280 285	
cca gca agc att ctg tgt ggc att gtg tcc gta aag cct aac gtg aag	912
Pro Ala Ser Ile Leu Cys Gly Ile Val Ser Val Lys Pro Asn Val Lys	
290 295 300	
gaa ttc aca gag acc tcg gcc att ttt gag gat ggg acc ata ttt gag	960
Glu Phe Thr Glu Thr Ser Ala Ile Phe Glu Asp Gly Thr Ile Phe Glu	
305 310 315 320	
ggc att gac tgt gta atc ttt gca aca ggg tat agt ttt gcc tac ccc	1008
Gly Ile Asp Cys Val Ile Phe Ala Thr Gly Tyr Ser Phe Ala Tyr Pro	
325 330 335	
ttc ctt gat gag tct atc atc aaa agc aga aac aat gag atc att tta	1056
Phe Leu Asp Glu Ser Ile Ile Lys Ser Arg Asn Asn Glu Ile Ile Leu	
340 345 350	
ttt aaa gga gta ttt cct cct cta ctt gag aag tca acc ata gca gtg	1104
Phe Lys Gly Val Phe Pro Pro Leu Leu Glu Lys Ser Thr Ile Ala Val	
355 360 365	
att ggc ttt gtc cag tcc ctt ggg gct gcc att ccc aca gtt gac ctc	1152
Ile Gly Phe Val Gln Ser Leu Gly Ala Ala Ile Pro Thr Val Asp Leu	
370 375 380	
cag tcc cgc tgg gca gca caa gta ata aag gga act tgt act ttg cct	1200
Gln Ser Arg Trp Ala Ala Gln Val Ile Lys Gly Thr Cys Thr Leu Pro	
385 390 395 400	
tct atg gaa gac atg atg aat gat att aat gag aaa atg gag aaa aag	1248
Ser Met Glu Asp Met Met Asn Asp Ile Asn Glu Lys Met Glu Lys Lys	
405 410 415	
cgc aaa tgg ttt ggc aaa agc gag acc ata cag aca gat tac att gtt	1296
Arg Lys Trp Phe Gly Lys Ser Glu Thr Ile Gln Thr Asp Tyr Ile Val	
420 425 430	

tat atg gat gaa ctc tcc tcc ttc att ggg gca aag ccc aac atc cca	1344
Tyr Met Asp Glu Leu Ser Ser Phe Ile Gly Ala Lys Pro Asn Ile Pro	
435 440 445	

tgg ctg ttt ctc aca gat ccc aaa ttg gcc atg gaa gtt tat ttt ggc	1392
Trp Leu Phe Leu Thr Asp Pro Lys Leu Ala Met Glu Val Tyr Phe Gly	
450 455 460	

cct tgt agt ccc tac cag ttt agg ctg gtg ggc cca ggg cag tgg cca	1440
Pro Cys Ser Pro Tyr Gln Phe Arg Leu Val Gly Pro Gly Gln Trp Pro	
465 470 475 480	

gga gcc aga aat gcc ata ctg acc cag tgg gac cgg tcg ttg aaa ccc	1488
Gly Ala Arg Asn Ala Ile Leu Thr Gln Trp Asp Arg Ser Leu Lys Pro	
485 490 495	

atg cag aca cga gtg gtc ggg aga ctt cag aag cct tgc ttc ttt ttc	1536
Met Gln Thr Arg Val Val Gly Arg Leu Gln Lys Pro Cys Phe Phe Phe	
500 505 510	

cat tgg ctg aag ctc ttt gca att cct att ctg tta atc gct gtt ttc	1584
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Leu Val Leu Thr	
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20 25 30																	
Lys Ser Asn Asp Ile Gly Gly Leu Trp Lys Phe Ser Asp His Ala Glu																	
35 40 45																	
Glu Gly Arg Ala Ser Ile Tyr Lys Ser Val Phe Ser Asn Ser Ser Lys																	
50 55 60																	
Glu Met Met Cys Phe Pro Asp Phe Pro Phe Pro Asp Asp Phe Pro Asn																	
65 70 75 80																	
Phe Met His Asn Ser Lys Ile Gln Glu Tyr Ile Ile Ala Phe Ala Lys																	
85 90 95																	
Glu Lys Asn Leu Leu Lys Tyr Ile Gln Phe Lys Thr Phe Val Ser Ser																	

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Gln	Val	Met	Ile	Ser	Ser	Arg	Ser	Gly	Ser	Trp	Val	Met	Ser	Arg	Val		
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Thr	Phe	Leu	Lys	Asn	Asn	Leu	Pro	Thr	Ala	Ile	Ser	Asp	Trp	Leu	Tyr		
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Arg	Lys	Trp	Phe	Gly	Lys	Ser	Glu	Thr	Ile	Gln	Thr	Asp	Tyr	Ile	Val		
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	450					455					460						
Pro	Cys	Ser	Pro	Tyr	Gln	Phe	Arg	Leu	Val	Gly	Pro	Gly	Gln	Trp	Pro		
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Ser Ile Arg Ser Cys Leu Glu Glu Gly Leu Glu Pro Thr Cys Phe Glu	
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Lys Ser Asn Asp Ile Gly Gly Leu Trp Lys Phe Ser Asp His Ala Glu	
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gag ggc agg gct agc att tac aaa tca gtc ttt tcc aac tct tcc aaa	192
Glu Gly Arg Ala Ser Ile Tyr Lys Ser Val Phe Ser Asn Ser Ser Lys	
50 55 60	
gag atg atg tgt ttc cca gac ttc cca ttt ccc gat gac ttc ccc aac	240
Glu Met Met Cys Phe Pro Asp Phe Pro Phe Pro Asp Asp Phe Pro Asn	
65 70 75 80	
ttt atg cac aac agc aag atc cag gaa tat atc att gca ttt gcc aaa	288
Phe Met His Asn Ser Lys Ile Gln Glu Tyr Ile Ile Ala Phe Ala Lys	
85 90 95	
gaa aag aac ctc ctg aag tac ata caa ttt aag aca ttt gta tcc agt	336
Glu Lys Asn Leu Leu Lys Tyr Ile Gln Phe Lys Thr Phe Val Ser Ser	
100 105 110	

gta aat aaa cat cct gat ttt gca act act ggc cag tgg gat gtt acc	384
Val Asn Lys His Pro Asp Phe Ala Thr Thr Gly Gln Trp Asp Val Thr	
115 120 125	
act gaa agg gat ggt aaa aaa gaa tcg gct gtc ttt gat gct gta atg	432
Thr Glu Arg Asp Gly Lys Lys Glu Ser Ala Val Phe Asp Ala Val Met	
130 135 140	
gtt tgt tcc gga cat cat gtg tat ccc aac cta cca aaa gag tcc ttt	480
Val Cys Ser Gly His His Val Tyr Pro Asn Leu Pro Lys Glu Ser Phe	
145 150 155 160	
cca gga cta aac cac ttt aaa ggc aaa tgc ttc cac agc agg gac tat	528
Pro Gly Leu Asn His Phe Lys Gly Lys Cys Phe His Ser Arg Asp Tyr	
165 170 175	
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Lys Glu Pro Gly Val Phe Asn Gly Lys Arg Val Leu Val Val Gly Leu	
180 185 190	
ggg aat tcg ggc tgt gat att gcc aca gaa ctc agc cgc aca gca gaa	624
Gly Asn Ser Gly Cys Asp Ile Ala Thr Glu Leu Ser Arg Thr Ala Glu	
195 200 205	
cag gtc atg atc agt tcc aga agt ggc tcc tgg gtg atg agc cgg gtc	672
Gln Val Met Ile Ser Ser Arg Ser Gly Ser Trp Val Met Ser Arg Val	
210 215 220	
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Trp Asp Asn Gly Tyr Pro Trp Asp Met Leu Leu Val Thr Arg Phe Gly	
225 230 235 240	
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Thr Phe Leu Lys Asn Asn Leu Pro Thr Ala Ile Ser Asp Trp Leu Tyr	
245 250 255	
gtg aag cag atg aat gca aga ttc aag cat gaa aac tat ggc ttg atg	816
Val Lys Gln Met Asn Ala Arg Phe Lys His Glu Asn Tyr Gly Leu Met	
260 265 270	
cct tta aat gga gtc ctg agg aaa gag cct gta ttt aac gat gag ctc	864
Pro Leu Asn Gly Val Leu Arg Lys Glu Pro Val Phe Asn Asp Glu Leu	
275 280 285	
cca gca agc att ctg tgt ggc att gtg tcc gta aag cct aac gtg aag	912
Pro Ala Ser Ile Leu Cys Gly Ile Val Ser Val Lys Pro Asn Val Lys	
290 295 300	

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Met	Gln	Thr	Arg	Val	Val	Gly	Arg	Leu	Gln	Lys	Pro	Cys	Phe	Phe	Phe	
			500					505					510			

cat	tgg	ctg	aag	ctc	ttt	gca	att	cct	att	ctg	tta	atc	gct	gtt	ttc	1584
His	Trp	Leu	Lys	Leu	Phe	Ala	Ile	Pro	Ile	Leu	Leu	Ile	Ala	Val	Phe	
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ctt	gtg	ttg	acc	taa												1599
Leu	Val	Leu	Thr													
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<212> PRT

<213> Homo sapiens

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Lys	Ser	Asn	Asp	Ile	Gly	Gly	Leu	Trp	Lys	Phe	Ser	Asp	His	Ala	Glu	
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Lys	Glu	Pro	Gly	Val	Phe	Asn	Gly	Lys	Arg	Val	Leu	Val	Val	Gly	Leu	
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Gln	Val	Met	Ile	Ser	Ser	Arg	Ser	Gly	Ser	Trp	Val	Met	Ser	Arg	Val	
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Val	Lys	Gln	Met	Asn	Ala	Arg	Phe	Lys	His	Glu	Asn	Tyr	Gly	Leu	Met
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Phe	Leu	Asp	Glu	Ser	Ile	Ile	Lys	Ser	Arg	Asn	Asn	Glu	Ile	Ile	Leu
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Phe	Lys	Gly	Val	Phe	Pro	Pro	Leu	Leu	Glu	Lys	Ser	Thr	Ile	Ala	Val
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Ile	Gly	Phe	Val	Gln	Ser	Leu	Gly	Ala	Ala	Ile	Pro	Thr	Val	Asp	Leu
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Gln	Ser	Arg	Trp	Ala	Ala	Gln	Val	Ile	Lys	Gly	Thr	Cys	Thr	Leu	Pro
385				390					395					400	
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Arg	Lys	Trp	Phe	Gly	Lys	Ser	Glu	Thr	Ile	Gln	Thr	Asp	Tyr	Ile	Val
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Tyr	Met	Asp	Glu	Leu	Ser	Ser	Phe	Ile	Gly	Ala	Lys	Pro	Asn	Ile	Pro
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Trp	Leu	Phe	Leu	Thr	Asp	Pro	Lys	Leu	Ala	Met	Glu	Val	Tyr	Phe	Gly
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Pro	Cys	Ser	Pro	Tyr	Gln	Phe	Arg	Leu	Val	Gly	Pro	Gly	Gln	Trp	Pro
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Gly	Ala	Arg	Asn	Ala	Ile	Leu	Thr	Gln	Trp	Asp	Arg	Ser	Leu	Lys	Pro
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Met	Gln	Thr	Arg	Val	Val	Gly	Arg	Leu	Gln	Lys	Pro	Cys	Phe	Phe	Phe
		500					505					510			
His	Trp	Leu	Lys	Leu	Phe	Ala	Ile	Pro	Ile	Leu	Leu	Ile	Ala	Val	Phe
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Leu	Val	Leu	Thr												
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<212> DNA

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6

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<212> PRT

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<223> Description of Artificial Sequence: HLFM03 -
Putative FAD binding domain.

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5

<210> 13

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<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: NADP+ binding
domain HLFM03

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5

<210> 14
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 <223> Description of Artificial Sequence: HFM 3 cDNA
 primer

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29

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